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Most Similar Matches in MEDLINE:

Score of self comparison: 79.7756

1		The use of multiple displacement amplified DNA as a control for methylation specific PCR, pyrosequencing, bisulfile sequencing and methylation specific restriction enzyme PCR.	Score: 94.14 Ratio:1.18
		S Hughes, JL Jones. BMC molecular biology, 2007, , , 8(): 91. PMID: 17939862	
2		Multiple displacement amplification prior to single nucleotide polymorphism genotyping in epidemiologic studies.	Score: 82.54 Ratio:1.03
		GJ Tranah, PJ Lescault, DJ Hunter, I De Vivo. Biotechnology letters, 2003, Jul, , 25(13): 1031-6. PMID: 12889810	
3		Single-molecule dilution and multiple displacement amolification for molecular haplotyping.	Score: 75.63 Ratio:0.95
		P Paul, J Apgar. BioTechniques, 2005, Apr., , 38(4): 553-4, 556, 558-9. PMID: 15884673	
4		Evaluation of whole-genome amplification using multiple-displacement amplification of a limited number of cells.	Score: 72 Ratio:0.9
		S Bashiardes, N Salame, PC Patsalis. Clinical chemistry and laboratory medicine: CCLM / FESCC, 2006, , , 44(9): 1158-60. PMID: 16958614	
5		Concurrent methylation of promoters from tumor associated genes predicts outcome to acute myeloid leukemia.	Score: 66.99 Ratio:0.84
		CJ Hess, A Errami, J Berkhof, F Denkers, GJ Ossenkoppele, AO Nygren, GJ Schuurhuis, Q Waisfisz. Leukemia lymphoma, 2008, Jun, , 49(6): 1132-41. PMID: 18569637	
6	800	Anchored multiplex amplification on a microelectronic chip array.	Score: 64.36 Ratio:0.81
		L Westin, X Xu, C Miller, L Wang, CF Edman, M Nerenberg. Nature biotechnology, 2000, Feb, , 18(2): 199-204. PMID: 10657128	
7	833	Analysis of DNA methylation by amplification of intermethylated sites (AIMS).	Score: 63.73 Ratio:0.8
		M Jordà, J Rodríguez, J Frigola, MA Peinado. Methods in molecular biology (Clifton, N.J.), 2009, , , 507(): 107-16. PMID: 18987810	
8	833	Quantitative high-throughput analysis of DNA methylation patterns by base-specific cleavage and mass spectrometry.	Score: 60.54 Ratio:0.76
		M Ehrich, MR Nelson, P Stanssens, M Zabeau, T Liloglou, G Xinarianos, CR Cantor, JK Field, D van den Boom. Proceedings of the National Academy of Sciences of the United S, 2005, Nov., 102(44): 15785-90. PMID: 16243968	
9		Strand displacement amplification: a versatile tool for molecular diagnostics.	Score: 60.3 Ratio:0.76
		TJ Hellyer, JG Nadeau. Expert review of molecular diagnostics, 2004, Mar, , 4(2): 251-61. PMID: 14995911	
10		Mutation detection in DNA isolated from serebrospinal fluid and urine: Clinical willity and pitfalls of multiple displacement amplification.	Score: 58.74 Ratio:0.74
		EH Rosenberg, EA Struys, K Hyland, B Plecko, PJ Waters, S Mercimek-Mahmutoglu, S Stockler-Ipsiroglu, RC Gallagher, G Scharer, JL Van Hove, C Jakobs, GS Salomons. Molecular genetics and metabolism, 2009, Aug, , 97(4): 312-4. PMID: 19501531	
11		Multiple displacement amplification commonises quantitative soalizats of metagenomes.	Score: 56.85 Ratio:0.71
		S Yilmaz, M Allgaier, P Hugenholtz. Nature methods, 2010, Dec, , 7(12): 943-4. PMID: 21116242	
12		Genome amplification of single sperm using multiple displacement amplification.	Score: 47.98 Ratio:0.6
		Z Jiang, X Zhang, R Deka, L Jin. Nucleic acids research, 2005, , , 33(10): e91. PMID: 15942023	
13	803	Investigation of genomic methylation states using methylation-specific and bisulfite sequencing polymerase chain reaction.	Score: 47.66 Ratio:0.6
		M Carless. Methods in molecular biology (Clifton, N.J.), 2009, , , 523(): 217-34. PMID: 19381936	

14		Multiple displacement amplification as a pre-polymerase chain reaction (pre-PCR) to process difficult to amplify samples and low copy number sequences from natural environments. JM Gonzalez, MC Portillo, C Saiz-Jimenez. Environmental microbiology, 2005, Jul., 7(7): 1024-8. PMID: 15946299	Score: 47.63 Ratio:0.6
15		Multiple displacement amplification products are compatible with recombination-based cioning.	Score: 47.37 Ratio:0.59
		MB Jakov, PD Kassner. BioTechniques, 2007, Jun, , 42(6): 706, 708. PMID: 17612292	
16		Ligation overcomes terminal underrepresentation in multiple displacement amplification of linear DNA.	Score: 47.37 Ratio:0.59
		S Panelli, G Damiani, L Espen, V Sgaramella. BioTechniques, 2005, Aug., 39(2): 174, 176, 178 passim. PMID: 16116788	
17		DNA simplification method tolerant to sample degradation.	Score: 47.05 Ratio:0.59
		G Wang, E Maher, C Brennan, L Chin, C Leo, M Kaur, P Zhu, M Rook, JL Wolfe, GM Makrigiorgos. Genome research, 2004, Nov., 14(11): 2357-66. PMID: 15520297	1440.0.33
18		Multiplex detection of CpG methylation using microarray combining with target-selection-padhock probe.	Score: 46.88 Ratio:0.59
		X Shi, C Tang, D Zhou, H Zhao, Z Lu. Clinica chimica acta; international journal of clinical chemist, 2010, Sep., 411(17-18): 1187-94. PMID: 20347753	
19		Quantitative analysis of DNA methylation after whole bisulfitume amolification of a minute amount of DNA from body fluids.	Score: 46.18 Ratio:0.58
		T Vaissière, C Cuenin, A Paliwal, P Vineis, G Hoek, M Krzyzanowski, L Airoldi, A Dunning, S Garte, P Hainaut, C Malaveille, K Overvad, F Clavel-Chapelon, J Linseisen, H Boeing, A Trichopoulou, D Trichopoulos, A Kaladidi, D Palli, V Krogh, R Tumino, S Panico, HB Bueno-De-Mesquita, PH Peeters, M Kumle, CA Gonzalez, C Martinez, M Dorronsoro, A Barricarte, C Navarro, JR Quiros, G Berglund, L Janzon, B Jarvholm, NE Day, TJ Key, R Saracci, R Kaaks, E Riboli, P Hainaut, Z Herceg. Epigenetics: official journal of the DNA Methylation Society, 2009, May, , 4(4): 221-30. PMID: 19458486	
Rel		ncy Threshold (Similarity ratio = 0.56). Entries above here have an unusual level of similarity	
20		Microarray-based method for detecting methylation changes of p16(Ink4a) gene 51-CpG islands in gastric carcinomas.	Score: 44.36
		P Hou, JY Shen, MJ Ji, NY He, ZH Lu. World journal of gastroenterology: WJG, 2004, Dec, , 10(24): 3553-8. PMID: 15534905	Ratio:0.56
21		Whole-genome multiple displacement amplification from single cells.	Score: 43.39
		C Spits, C Le Caignec, M De Rycke, L Van Haute, A Van Steirteghem, I Liebaers, K Sermon. Nature protocols, 2006, , , 1(4): 1965-70. PMID: 17487184	Ratio:0.54
22	833	Combining nucleic sold amplification and detection.	Score: 43.04 Ratio:0.54
		B Schweitzer, S Kingsmore. Current opinion in biotechnology, 2001, Feb., 12(1): 21-7. PMID: 11167068	Rano.o.54
23		Towards the analysis of the genomes of single cells; further characterisation of the multiple displacement amplification.	Score: 42.56
		S Panelli, G Damiani, L Espen, G Micheli, V Sgaramella. Gene, 2006, May, , 372(): 1-7. PMID: 16564650	Ratio:0.53
24		Nucleic acid isothermal amplification technologies: a review.	Score: 42.15
		P Gill, A Ghaemi. Nucleosides, nucleotides nucleic acids, 2008, Mar, , 27(3): 224-43. PMID: 18260008	Ratio:0.53
25		Specific and complete human genome amplification with improved yield achieved by phi29 DNA polymerase and a novel primer at elevated	Score: 41.9
20		O Alsmadi, F Alkayal, D Monies, BF Meyer, BMC research notes, 2009, , , 2(): 48. PMID: 19309528	Ratio:0.53
26		Assessment of whole genome amplification-induced bias through high-throughput, massively parallel whole genome sequencing.	Score: 41.28
20		R Pinard, A de Winter, GJ Sarkis, MB Gerstein, KR Tartaro, RN Plant, M Egholm, JM Rothberg, JH Leamon. BMC genomics, 2006, , , 7(): 216.	Ratio:0.52
		PMID: 16928277	
27		Multiple displacement amplification to create a long-lasting source of DNA for genetic studies.	Score: 40.81 Ratio:0.51
		L Lovmar, AC Syvänen. Human mutation, 2006, Jul., 27(7): 603-14. PMID: 16786504	
28		Genome-wide DNA mothylation profiles in prothelial carcinomas and prothelia at the precancerous stage.	Score: 40.45 Ratio:0.51
		N Nishiyama, E Arai, Y Chihara, H Fujimoto, F Hosoda, T Shibata, T Kondo, T Tsukamoto, S Yokoi, I Imoto, J Inazawa, S Hirohashi, Y Kanai. Cancer science, 2010, Jan, , 101(1): 231-40. PMID: 19775289	***************************************
29		[Quantitative microarray-based DNA methylation analysis of E-cadherin gene promoter in acute leukemia].	Score: 39.24
		BA Chen, F Zhang, Y Wang, WL Zheng, J Du, C Gao, JH Ding, YY Sun, J Cheng, J Wang, G Zhao, NN Chen, ZH Lu. Zhonghua zhong liu za zhi [Chinese journal of oncology], 2007, Jan, , 29(1): 41-4. PMID: 17575692	Ratio:0.49
30		Screening hypermethylated regions by methylation-sensitive single-strand conformational polymorphism.	Score: 38.81
		H Kinoshita, Y Shi, C Sandefur, DF Jarrard. Analytical biochemistry, 2000, Feb., 278(2): 165-9. PMID: 10660458	Ratio:0.49
		, , , , , , , , , , , , , , , , , , ,	

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31	3003	Multiple displacement amplification as an aid in checkerboard DNA-DNA hybridization.	Score: 37.63 Ratio:0.47
		F Teles, AD Haffajee, SS Socransky. Oral microbiology and immunology, 2007, Apr., 22(2): 118-25. PMID: 17311635	
32		Genomic DNA amplification by the multiple displacement amplification (MDA) method.	Score: 35.97 Ratio:0.45
		RS Lasken. Biochemical Society transactions, 2009, Apr., 37(Pt 2): 450-3. PMID: 19290880	
33		Comprehensive human genome amplification using multiple displacement amplification.	Score: 33.82 Ratio:0.42
		FB Dean, S Hosono, L Fang, X Wu, AF Faruqi, P Bray-Ward, Z Sun, Q Zong, Y Du, J Du, M Driscoll, W Song, SF Kingsmore, M Egholm, RS Lasken. Proceedings of the National Academy of Sciences of the United S, 2002, Apr., 99(8): 5261-6. PMID: 11959976	
34		Molecular crowding increases the amplification success of multiple displacement amplification and short tandem repeat genotyping.	Score: 33.17 Ratio:0.42
		KN Ballantyne, RA van Oorschot, RJ Mitchell, I Koukoulas. Analytical biochemistry, 2006, Aug, , 355(2): 298-303. PMID: 16737679	
35		Quantitative DNA methylation analysis by fluorescent polymerase chain reaction single-strand conformation polymorphism using an automated DNA sequences.	Score: 32.71 Ratio:0.41
		H Suzuki, F Itoh, M Toyota, T Kikuchi, H Kakiuchi, Y Hinoda, K Imai. Electrophoresis, 2000, Mar, , 21(5): 904-8. PMID: 10768775	
36		Isothermal target and signaling probe amplification method, based on a combination of an isothermal chain amplification technique and a fluorescence resource energy transfer cycling probe technology.	Score: 32.48 Ratio:0.41
		C Jung, JW Chung, UO Kim, MH Kim, HG Park. Analytical chemistry, 2010, Jul, , 82(14): 5937-43. PMID: 20575518	Ttalio i i i
37		Amplification of fungal genomes using multiple displacement amplification.	Score: 31.85 Ratio:0.4
		SJ Foster, BJ Monahan. Methods in molecular biology (Clifton, N.J.), 2010, , , 638(): 175-85. PMID: 20238269	Rano.o.+
38		Sequencing of the large deDNA genome of Orycles rhinoceros nudivirus using multiple displacement amplification of nanogram amounts of virus DNA.	Score: 31.63 Ratio:0.4
		Y Wang, RG Kleespies, MB Ramle, JA Jehle. Journal of virological methods, 2008, Sep., 152(1-2): 106-8. PMID: 18598718	Rano.o.+
39		Aberrant methylation of multiple genes in neuroblastic tumours, relationship with MYCN amplification and allelic status at 1p.	Score: 31.59 Ratio:0.4
		P Gonzalez-Gomez, MJ Bello, J Lomas, D Arjona, ME Alonso, C Amiñoso, I Lopez-Marin, NP Anselmo, JL Sarasa, M Gutierrez, C Casartelli, JA Rey. European journal of cancer (Oxford, England: 1990), 2003, Jul., 39(10): 1478-85. PMID: 12826052	
40		Assessment of multiple displacement amplification for polymorphism discovery and haplotype determination at a highly polymorphic locus,	Score: 30.78 Ratio:0.39
		MCIR. KK Murthy, VS Mahboubi, A Santiago, MT Barragan, R Knöll, HP Schultheiss, DT O'Connor, NJ Schork, BK Rana. Human mutation, 2005, Aug., 26(2): 145-52. PMID: 15957185	Kano.o.39
41		Whole genome amplification of plasma-circulating DNA enables expanded sevening for allelic imbalance in plasma.	Score: 30.78 Ratio:0.39
		J Li, L Harris, H Mamon, MH Kulke, WH Liu, P Zhu, G Mike Makrigiorgos. The Journal of molecular diagnostics: JMD, 2006, Feb, , 8(1): 22-30. PMID: 16436631	Kano.0.39
42		Preimplantation genetic diagnosis of Marian syndrome using multiple displacement amplification.	Score: 29.79 Ratio:0.37
		B Lledó, J Ten, FM Galán, R Bernabeu. Fertility and sterility, 2006, Oct, , 86(4): 949-55. PMID: 17027361	Rano.0.57
43		Nanoliter reactors improve multiple displacement annolification of genomes from single cells.	Score: 29.3 Ratio:0.37
		Y Marcy, T Ishoey, RS Lasken, TB Stockwell, BP Walenz, AL Halpern, KY Beeson, SM Goldberg, SR Quake. PLoS genetics, 2007, Sep., 3(9):	Kano.0.37
	888	1702-8. PMID: 17892324	Saara, 20.02
44	888	Mothylation-specific PCR.	Score: 29.02 Ratio:0.36
	9999	JD Licchesi, JG Herman. Methods in molecular biology (Clifton, N.J.), 2009, , , 507(): 305-23. PMID: 18987823	g 20.01
45		Sequence quality is maintained after multiple displacement amplification of non-invasively obtained macaque semen DNA.	Score: 28.91 Ratio:0.36
		O Andrés, AC Rönn, A Ferrando, M Bosch, X Domingo-Roura. Biotechnology journal, 2006, Apr, , 1(4): 466-9. PMID: 16892275	
46		Effects of electron-beam irradiation on whole genome amplification.	Score: 28.89 Ratio:0.36
		AW Bergen, Y Qi, KA Haque, RA Welch, M Garcia-Closas, SJ Chanock, J Vaught, PE Castle. Cancer epidemiology, biomarkers prevention: a publication of, 2005, Apr., 14(4): 1016-9. PMID: 15824182	
47		Decreasing amplification bias associated with multiple displacement amplification and short tandem repeat genotyping.	Score: 28.78 Ratio:0.36
		KN Ballantyne, RA van Oorschot, I Muharam, A van Daal, R John Mitchell. Analytical biochemistry, 2007, Sep., 368(2): 222-9. PMID: 17583668	
48		Isothermal multiple displacement amplification, a highly reliable approach for generating unlimited high molecular weight genomic ONA from clinical specimens.	Score: 28.63 Ratio:0.36
		R Luthra, LJ Medeiros. The Journal of molecular diagnostics: JMD, 2004, Aug, , 6(3): 236-42. PMID: 15269301	
49		Use of multiple displacement amplification to increase the detection and genotyping of trypanosoma species samples immobilized on FTA filters.	Score: 28.43 Ratio:0.36

		LJ Morrison, G McCormack, L Sweeney, AC Likeufack, P Truc, CM Turner, A Tait, A MacLeod. The American journal of tropical medicine and hygiene, 2007, Jun, , 76(6): 1132-7. PMID: 17556624	
50	800	Efficient isothernal amplitication of the entire genome from single cells.	Score: 28.15 Ratio:0.35
		KV Schowalter, J Fredrickson, AR Thornhill. Methods in molecular medicine, 2007, , , 132(): 87-99. PMID: 17876078	Tunio 10132
51	800	The use of multiple displacement amplification to amplify complex DNA libraries	Score: 28.11 Ratio:0.35
		MJ Fullwood, JJ Tan, PW Ng, KP Chiu, J Liu, CL Wei, Y Ruan. Nucleic acids research, 2008, Mar, , 36(5): e32. PMID: 18285362	Raio.o.33
52	800	Single-cell genomic sequencing using Multiple Displacement Amplification	Score: 27.31 Ratio:0.34
		RS Lasken. Current opinion in microbiology, 2007, Oct, , 10(5): 510-6. PMID: 17923430	Tutto.o.s
53	823	Multiple sample amplification and genotyping integrated on a single electronic microarray.	Score: 27.11 Ratio:0.34
		Y Huang, J Shirajian, A Schroder, Z Yao, T Summers, D Hodko, R Sosnowski. Electrophoresis, 2004, Oct, , 25(18-19): 3106-16. PMID: 15472977	14401013
54		Whole genome amphification of the rust Puccinia striliformis f. sp., tritici from single spores.	Score: 26.68 Ratio:0.33
		Y Wang, M Zhu, R Zhang, H Yang, Y Wang, G Sun, S Jin, T Hsiang. Journal of microbiological methods, 2009, May, , 77(2): 229-34. PMID:	Kauo.0.33
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55	800	In-gel multiple displacement amplification of long DNA fragments diluted to the single molecule level.	Score: 26.44 Ratio:0.33
		Y Michikawa, K Sugahara, T Suga, Y Ohtsuka, K Ishikawa, A Ishikawa, N Shiomi, T Shiomi, M Iwakawa, T Imai. Analytical biochemistry, 2008, Dec., 383(2): 151-8. PMID: 18768135	
56		Multiple displacement amplification improves PGD for fragile X syndrome.	Score: 26.44
		P Burlet, N Frydman, N Gigarel, V Kerbrat, G Tachdjian, E Feyereisen, JP Bonnefont, R Frydman, A Munnich, J Steffann. Molecular human	Ratio:0.33
	9222	reproduction, 2006, Oct, , 12(10): 647-52. PMID: 16896070	g 2630
57	80	WEIHWARDIN GOILES IN OISOST WILKEL	Score: 26.39 Ratio:0.33
	1222	N Buyru, J Altinisik, F Ozdemir, S Demokan, N Dalay. Cancer investigation, 2009, Mar, , 27(3): 307-12. PMID: 19194828	
58	800	Plasmodium vivax: microsatellite analysis of multiple-clone infections.	Score: 25.6 Ratio:0.32
	,,,,,	T Havryliuk, P Orjuela-Sánchez, MU Ferreira. Experimental parasitology, 2008, Dec, , 120(4): 330-6. PMID: 18801362	
59	80	Multiple displacement amplification, a powerful tool for molecular genetic analysis of powdery mildew funci.	Score: 25.59 Ratio:0.32
		D Fernández-Ortuño, JA Torés, A de Vicente, A Pérez-García. Current genetics, 2007, Mar, , 51(3): 209-19. PMID: 17256172	
60	80	SNP-based chromosomal copy number ascertainment following multiple displacement whole-genome amplification.	Score: 24.97 Ratio:0.31
		JJ Corneveaux, MC Kruer, D Hu-Lince, KE Ramsey, VL Zismann, DA Stephan, DW Craig, MJ Huentelman. BioTechniques, 2007, Jan., 42(1): 77-83. PMID: 17269488	
61		Whole-metagenome amplification of a microbial community associated with scleractinian coral by multiple displacement amplification using ph/29 polymerase.	Score: 24.19 Ratio:0.3
		H Yokouchi, Y Fukuoka, D Mukoyama, R Calugay, H Takeyama, T Matsunaga. Environmental microbiology, 2006, Jul, , 8(7): 1155-63. PMID: 16817924	
62		Singleton birth after preimplautation, genetic diagnosis for Huntington disease using whole genome amplification.	Score: 23.67 Ratio:0.3
		JF Chow, WS Yeung, EY Lau, ST Lam, T Tong, EH Ng, PC Ho. Fertility and sterility, 2009, Aug, , 92(2): 828.e7-10. PMID: 19515365	
63	80	Multiple displacement amplification for complex mixtures of DNA fragments.	Score: 23.64 Ratio:0.3
		M Shoaib, S Baconnais, U Mechold, E Le Cam, M Lipinski, V Ogryzko. BMC genomics, 2008, , , 9(): 415. PMID: 18793430	
64		Strand displacement amplification and fluorescence polarization.	Score: 23.4 Ratio:0.29
		D Seckinger. Clinical chemistry, 1996, Oct, , 42(10): 1720. PMID: 8855164	
65		Whole-genome amplification of oral rinse self-collected DNA in a population-based case-control study of breast cancer.	Score: 23.32 Ratio:0.29
		X Liang, A Trentham-Dietz, L Titus-Emstoff, PA Newcomb, RA Welch, AA Hutchinson, JM Hampton, CB Sutcliffe, JL Haines, KM Egan. Cancer epidemiology, biomarkers prevention: a publication of, 2007, Aug., 16(8): 1610-4. PMID: 17684135	
66	800	Amplifying whole insect genomes with multiple displacement amplification.	Score: 23.22 Ratio:0.29
		N Gorrochotegui-Escalante, WC Black. Insect molecular biology, 2003, Apr., , 12(2): 195-200. PMID: 12653941	
67	800	Clinical application of multiple displacement amplification in preimplantation genetic diagnosis.	Score: 22.11 Ratio:0.28
		A Hellani, S Coskun, A Tbakhi, S Al-Hassan. Reproductive biomedicine online, 2005, Mar, , 10(3): 376-80. PMID: 15820046	

68	88	Multiple displacement ampitification on single cell and possible PGD applications.	Score: 21.97 Ratio:0.28
		A Hellani, S Coskun, M Benkhalifa, A Tbakhi, N Sakati, A Al-Odaib, P Ozand. Molecular human reproduction, 2004, Nov., , 10(11): 847-52. PMID: 15465849	
69		Something from (almost) nothing: the impact of multiple displacement amplification on microbial ecology.	Score: 21.28 Ratio:0.27
		EK Binga, RS Lasken, JD Neufeld. The ISME journal, 2008, Mar., 2(3): 233-41. PMID: 18256705	
70		Evidence of BPV16 integration in low- and high-grade cervical lesions that regress demonstrated by multiple displacement amplification and Southern blot hybridisation.	Score: 21.28 Ratio:0.27
		MF Evans, CS Adamson, K Cooper. Journal of clinical pathology, 2008, Apr., 61(4): 541-3. PMID: 18006667	
71		Development of microbial genome-probing microarrays using digital multiple displacement amplification of uncultivated microbial single cells.	Score: 21.28 Ratio:0.27
		HW Chang, Y Sung, KH Kim, YD Nam, SW Roh, MS Kim, CO Jeon, JW Bae. Environmental science technology, 2008, Aug, , 42(16): 6058-64. PMID: 18767666	
72		[Evaluation of the fidelity of multiple displacement amplification from small number of cells].	Score: 20.94 Ratio:0.26
		J Ling, C Fang, Y Xu, G Zhuang, B Cao. Zhonghua yi xue yi chuan xue za zhi = Zhonghua yixue yichuanxue, 2010, Feb, , 27(1): 42-6. PMID: 20140866	
73		Comparison at viold and centivoice performance of multiple displacement amplification and OmniPicz whole genome amplified DNA generated from multiple DNA generated from multiple DNA generated.	Score: 20.66 Ratio:0.26
		AW Bergen, KA Haque, Y Qi, MB Beerman, M Garcia-Closas, N Rothman, SJ Chanock. Human mutation, 2005, Sep., 26(3): 262-70. PMID: 16086324	
74		Use of multiple displacement amplification to amplify genomic DNA before sequencing of the alpha and beta haemoslobin genes.	Score: 20.14 Ratio:0.25
		M Mai, JD Hoyer, RF McClure. Journal of clinical pathology, 2004, Jun, , 57(6): 637-40. PMID: 15166271	
75		Use of the restriction enzyme Aval and exo- Bet polymerase in strand displacement amplification.	Score: 20.05 Ratio:0.25
		MA Milla, PA Spears, RE Pearson, GT Walker. BioTechniques, 1998, Mar, , 24(3): 392-6. PMID: 9526646	
76		(Principle and application of strand displacement amolification method).	Score: 20.05 Ratio:0.25
		N Sawada. Rinshō Biseibutsu Jinsoku Shindan Kenkyūkai shi = JARMAM : Jour, 2003, , , 14(1): 31-7. PMID: 14984305	
77		Multiple recurrent genetic events converge on control of histone lysine methylation in medulloblastoms.	Score: 19.89 Ratio:0.25
		PA Northcott, Y Nakahara, X Wu, L Feuk, DW Ellison, S Croul, S Mack, PN Kongkham, J Peacock, A Dubuc, YS Ra, K Zilberberg, J McLeod, SW Scherer, J Sunil Rao, CG Eberhart, W Grajkowska, Y Gillespie, B Lach, R Grundy, IF Pollack, RL Hamilton, T Van Meter, CG Carlotti, F Boop, D Bigner, RJ Gilbertson, JT Rutka, MD Taylor. Nature genetics, 2009, Apr., 41(4): 465-72. PMID: 19270706	
78		Displacement synthesis of globin complementary LNA: evidence for sequence amplification.	Score: 19.53 Ratio:0.24
		JW Gaubatz, GV Paddock. Biochimica et biophysica acta, 1985, Jun, , 825(2): 175-87. PMID: 2988627	
79		Multiple displacement amplification for malaria parasite DNA	Score: 18.58 Ratio:0.23
		Y Wang, S Nair, F Nosten, TJ Anderson. The Journal of parasitology, 2009, Feb, , 95(1): 253-5. PMID: 18601578	
80		Genomic DNA amplification from a single bacterium.	Score: 18.29 Ratio:0,23
		A Raghunathan, HR Ferguson, CJ Bornarth, W Song, M Driscoll, RS Lasken. Applied and environmental microbiology, 2005, Jun, , 71(6): 3342-7. PMID: 15933038	Radio.0.23
81		Structure, amplification and methylation of omithine decarboxylase genes in human malignant cells.	Score: 17.68 Ratio:0.22
		J Jänne, L Alhonen, A Hirvonen, J Wahlfors, R Sinervirta, T Eloranta, E Hölttä, A Kallio. Advances in experimental medicine and biology, 1988, , , 250(): 253-60. PMID: 3076324	Kauo.0.22
82		Methylome profiling of cancer cells by amplification of inter-methylated sites (AIMS).	Score: 17.51 Ratio:0.22
		J Frigola, M Ribas, RA Risques, MA Peinado. Nucleic acids research, 2002, Apr., 30(7): e28. PMID: 11917034	Kano.0.22
83		Multiple methylation and bacterial adaptation.	Score: 17.05 Ratio:0.21
		J Armitage. Nature, 1981, Jan, , 289(5794): 121-2. PMID: 7453816	
84		Optimization and evaluation of single-cell whole-genome multiple displacement amplification.	Score: 17.02 Ratio:0.21
		C Spits, C Le Caignec, M De Rycke, L Van Haute, A Van Steirteghem, I Liebaers, K Sermon. Human mutation, 2006, May, , 27(5): 496-503. PMID: 16619243	
85		Multiple displacement amplification as a pre-polymerase chain reaction (pre-PCR) to detect ultra low population of Ralstonia solanaceanum (Smith 1896) Yabuchi et al. (1996).	Score: 16.87 Ratio:0.21
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